

SEQUENCE LISTING

<110> Tsuji, Takashi
Tezuka, Katsunari
Hori, Nobuaki

<120> HUMAN MONOCLONAL ANTIBODY AGAINST A
COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
PHARMACEUTICAL USE THEREOF

<130> 06501-079001

<140> US 09/859,053
<141> 2001-05-16

<150> JP 2001-99508
<151> 2001-03-30

<150> JP 2000-147116
<151> 2000-05-18

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<222> (69)...(1478)

<221> 3'UTR
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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala				
-15		-10		
aca gga gcc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg				158
Thr Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val				
-5	1	5	10	
aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac				206
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr				
15	20	25		
acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc cct gga caa				254
Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln				
30	35	40		
ggg ctt gag tgg atg gga tgg atc aac cct cac agt ggt ggc aca aac				302
Gly Leu Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn				
45	50	55		
tat gca cag aag ttt cag ggc agg gtc acc atg acc agg gac acg tcc				350
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser				
60	65	70	75	
atc agc aca gcc tac atg gag ctg agc agg ctg aga tcc gac gac acg				398
Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr				
80	85	90		
gcc gtg tat tac tgt gcg agg acg tat tac tat gat agt agt ggt tat				446
Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr				
95	100	105		
tac cat gat gct ttt gat atc tgg ggc caa ggg aca atg gtc acc gtc				494
Tyr His Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val				
110	115	120		
tct tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gcg ccc tgc				542
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys				
125	130	135		
tcc agg agc acc tcc gag agc aca gcg gcc ctg ggc tgc ctg gtc aag				590
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys				
140	145	150	155	
gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gct ctg				638
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu				
160	165	170		
acc agc ggc gtg cac acc ttc cca gct gtc cta cag tcc tca gga ctc				686
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu				
175	180	185		

tac tcc ctc agc agc gtg gtg acc gtc ccc tcc agc aac ttc ggc acc Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr 190 195 200	734
cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc aag gtg Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val 205 210 215	782
gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc cca Asp Lys Thr Val Glu Arg Lys Cys Val Glu Cys Pro Pro Cys Pro 220 225 230 235	830
gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 240 245 250	878
aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 255 260 265	926
gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val 270 275 280	974
gac ggc gtg gag gtg cat aat gcc aag aca aag cca ccg gag gag cag Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln 285 290 295	1022
ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac cag Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln 300 305 310 315	1070
gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly 320 325 330	1118
ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro 335 340 345	1166
cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr 350 355 360	1214
aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser 365 370 375	1262
gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 380 385 390 395	1310
aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 400 405 410	1358
agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc	1406

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 415 420 425
 tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag 1454
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 430 435 440
 agc ctc tcc ctg tct ccg ggt aaa tgagtgccac ggccggcaag ccccccgtcc 1508
 Ser Leu Ser Leu Ser Pro Gly Lys
 445 450
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 20 25 30
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 35 40 45
 Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala
 65 70 75 80
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Thr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His
 115 120 125
 Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290	295	300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg	Glu Glu Gln Phe Asn	
305	310	315
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp		320
325	330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro		
340	345	350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu		
355	360	365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn		
370	375	380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
385	390	395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr		400
405	410	415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
420	425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
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Ser Leu Ser Pro Gly Lys		
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<222> (39) ... (746)

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<222> (750) ... (974)

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<222> (39) ... (104)

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										-20

gct cag ctc ctg ggg ctc ctg ctg tgg ttc cca ggt tcc aga tgc	104		
Ala Gln Leu Leu Gly Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys			
-15	-10	-5	

gac atc cag atg acc cag tct cca tct tcc gtg tct gca tct gta gga	152			
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly				
1	5	10	15	

gac aga gtc acc atc act tgt cgg gcg agt cag ggt att agc agg ttg	200
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Leu	

20	25	30	
tta gcc tgg tat cag cag aaa cca ggg aaa gcc cct aaa ctc ctg atc Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 35	40	45	248
tat gtt gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50	55	60	296
agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65	70	75	344
gaa gat ttt gca act tac tat tgt caa cag gct aac agt ttc ccg tgg Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp 85	90	95	392
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 100	105	110	440
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115	120	125	488
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130	135	140	536
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145	150	155	584
gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165	170	175	632
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gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195	200	205	728
ttc aac agg gga gag tgt tagaggaga agtgccccca cctgctcctc Phe Asn Arg Gly Glu Cys 210			776
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35 40 45
Gln Gly Ile Ser Arg Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Ala Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205
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210 215 220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<221> CDS
<222> (94) ... (1503)

<221> 3'UTR
<222> (1507) ... (1708)

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<221> misc_feature
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 tcagtgatca ggactgagca cacaggactc acc atg gag ttg ggg ctg agc tgg 114
 Met Glu Leu Gly Leu Ser Trp
 -15

gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag ctg 162
 Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu
 -10 -5 1

gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga ctc 210
 Val Glu Ser Gly Gly Leu Val Gln Pro Gly Ser Leu Arg Leu
 5 10 15 20

tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac tgg 258
 Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp
 25 30 35

gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att ggt 306
 Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Gly
 40 45 50

act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc acc 354
 Thr Ala Gly Asp Thr Tyr Phe Pro Ser Val Lys Gly Arg Phe Thr
 55 60 65

atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac agc 402
 Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
 70 75 80

ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aat agg 450
 Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Asn Arg
 85 90 95 100

aag gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg ggc 498
 Lys Val Thr His Glu His Tyr Tyr Tyr Gly Met Asp Val Trp Gly
 105 110 115

caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 546
 Gln Gly Thr Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 120 125 130

gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca gcg 594
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 135 140 145

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 642
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 150 155 160

tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct 690
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175 180

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 738
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 185 190 195

ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His 200 205 210	786
aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys 215 220 225	834
gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc Val Glu Cys Pro Pro Cys Pro Ala Pro Val Ala Gly Pro Ser Val 230 235 240	882
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cggt acc Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr 245 250 255 260	930
cct gag gtc acg tgc gtg gtg gac gtg agc cac gaa gac ccc gag Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu 265 270 275	978
gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys 280 285 290	1026
aca aag cca cgg gag gag cag ttc aac acg acg ttc cgt gtg gtc acg Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser 295 300 305	1074
gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys 310 315 320	1122
tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile 325 330 335 340	1170
tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro 345 350 355	1218
cca tcc cgg gag gag atg acc aag aac cag gtc acg ctg acc tgc ctg Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu 360 365 370	1266
gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn 375 380 385	1314
ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser 390 395 400	1362
gac ggc tcc ttc ctc tac agc aag ctc acc gtg gac aag agc agg Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg 405 410 415 420	1410

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg		1458
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
425	430	435
cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa		1503
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
440	445	450
tgagtgccac ggccggcaag ccccgctcc ccaggctctc ggggtcggt gaggatgctt		1563
ggcacgtacc ccgtgtacat acttcccagg caccagcat gaaaataaag caccagcgc		1623
tgccctgggc ccctgcnaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa		1683
aaaaaaaaaa aatctctgcg gccgc		1708
<210> 32		
<211> 470		
<212> PRT		
<213> Homo sapiens		
<400> 32		
Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu Gly		
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Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln		
20 25 30		
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe		
35 40 45		
Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu		
50 55 60		
Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly		
65 70 75 80		
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser		
85 90 95		
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr		
100 105 110		
Tyr Cys Val Arg Asp Asn Arg Lys Val Thr His Glu His Tyr Tyr Tyr		
115 120 125		
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
130 135 140		
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg		
145 150 155 160		
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr		
165 170 175		
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser		
180 185 190		
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser		
195 200 205		
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr		
210 215 220		
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys		
225 230 235 240		
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro		
245 250 255		
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp		
260 265 270		
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		
275 280 285		
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly		
290 295 300		

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 325 330 335
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 340 345 350
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 355 360 365
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 370 375 380
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 33

<211> 948

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1) ... (27)

<221> CDS

<222> (28) ... (735)

<221> 3'UTR

<222> (739) ... (948)

<221> sig_peptide

<222> (28) ... (87)

<221> misc_feature

<222> (1) ... (948)

<223> n = A, T, C or G

<400> 33

gaattcgcag tgccatgaca ccacgcc atg gaa acc cca gcg cag ctt ctc ttc
 Met Glu Thr Pro Ala Gln Leu Leu Phe 54
 -20 -15

ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg ttg acg 102
 Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr
 -10 -5 1 5

cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc 150
 Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
 10 15 20

tcc tgc agg gcc agt cag aat att aga agc agc tac tta gcc tgg tac Ser Cys Arg Ala Ser Gln Asn Ile Arg Ser Ser Tyr Leu Ala Trp Tyr 25 30 35	198
cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc tat ggt gca tcc Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser 40 45 50	246
agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg tct ggg Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly 55 60 65	294
aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat ttt gca Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala 70 75 80 85	342
gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt ttt ggc Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser Phe Gly 90 95 100	390
cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca tct gtc Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val 105 110 115	438
ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser 120 125 130	486
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln 135 140 145	534
tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val 150 155 160 165	582
aca gag cag gac aag gac agc acc tac agc ctc agc agc acc ctg Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu 170 175 180	630
acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu 185 190 195	678
gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg 200 205 210	726
gga gag tgt tagagggaga antgccccca cctgctcctc agttccagcc Gly Glu Cys 215	775
tgacccccc ccatcccttg gcctctgacc cttttccac aggggaccta cccctattgc ggtcctccag ctcatcttc acctcacccc cctcctcctc cttggcttta attatgctaa tgttggagga gaatgaataa ataaagtcaa tcttgcacc tgtgaaaaaaa aaa	835 895 948

<210> 34

<211> 236

<212> PRT

<213> Homo sapiens

<400> 34

Met	Glu	Thr	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1						5			10				15		
Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser
		20						25					30		
Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Asn
			35					40			45				
Ile	Arg	Ser	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala
					50			55			60				
Pro	Gly	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro
		65				70			75				80		
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
			85					90					95		
Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Phe
			100					105				110			
Gly	Ser	Ser	Pro	Met	Cys	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile
			115					120				125			
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
			130					135			140				
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
	145				150				155				160		
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
			165					170				175			
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
		180						185			190				
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
		195						200			205				
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
		210						215			220				
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
		225				230				235					

<210> 35

<211> 1673

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1) ... (95)

<221> CDS

<222> (96) ... (1505)

<221> 3'UTR

<222> (1509) ... (1673)

<221> sig_peptide

<222> (96) ... (152)

<400> 35

gaattcgcag tgccatgaca ccacgggtgga gccccagcct tgggattccc aagtgtttgt

60

atccagtgat caggactgaa cacacaggac tcacc atg gag ttg ggg ctg agc Met Glu Leu Gly Leu Ser -15	113
tgg gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag Trp Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln -10 -5 1	161
ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg 5 10 15	209
ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His 20 25 30 35	257
tgg gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att Trp Val Arg Gln Ala Thr Gly Lys Leu Glu Trp Val Ser Ala Ile 40 45 50	305
ggt act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe 55 60 65	353
acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn 70 75 80	401
agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aag Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Lys 85 90 95	449
agg acg gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg Arg Thr Val Thr His Glu His Tyr Tyr Tyr Gly Met Asp Val Trp 100 105 110 115	497
ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro 120 125 130	545
tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr 135 140 145	593
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acc Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 150 155 160	641
gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 165 170 175	689
gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 180 185 190 195	737
gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat	785

Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp
					200			205						210	
cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aca	gtt	gag	cgc	aaa	tgt
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys
					215			220						225	
tgt	gtc	gag	tgc	cca	cgc	tgc	cca	gca	cca	cct	gtg	gca	gga	ccg	tca
Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser
					230			235						240	
gtc	ttc	ctc	tcc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
					245			250						255	
acc	cct	gag	gtc	acg	tgc	gtg	gtg	gac	gtg	agc	cac	gaa	gac	ccc	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
					260			265						275	
gag	gtc	cag	tcc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
					280			285						290	
aag	aca	aag	cca	cg	gag	gag	cag	ttc	aac	agc	acg	ttc	cgt	gtg	gtc
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val
					295			300						305	
agc	gtc	ctc	acc	gtt	gtg	cac	cag	tgg	ctg	aac	ggc	aag	gag	tac	
Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
					310			315						320	
aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	cca	gcc	ccc	atc	gag	aaa	acc
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
					325			330						335	
atc	tcc	aaa	acc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg
Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
					340			345						355	
ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
					360			365						370	
ctg	gtc	aaa	ggc	tcc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
					375			380						385	
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	aca	cct	ccc	atg	ctg	gac
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp
					390			395						400	
tcc	gac	ggc	tcc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
					405			410						415	
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala

420

425

430

435

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1505
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 440 445 450

tgagtgccac ggccggcaag ccccccgtcc ccaggctctc ggggtcgctt gaggatgctt 1565
 ggcacgtacc ccgtgtacat acttcccagg caccagcat ggaaataaaag caccagcgc 1625
 tgccctggc ccctgcgaaa aaaaaaaaaa aaaaaatctct gcgccgc 1673

<210> 36

<211> 470

<212> PRT

<213> Homo sapiens

<400> 36

Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu Gly
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 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr
 100 105 110
 Tyr Cys Val Arg Asp Lys Arg Thr Val Thr His Glu His Tyr Tyr Tyr
 115 120 125
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

	325	330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro			
	340	345	350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu			
	355	360	365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn			
	370	375	380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile			
	385	390	395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr			
	405	410	415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys			
	420	425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys			
	435	440	445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu			
	450	455	460
Ser Leu Ser Pro Gly Lys			
	465	470	

<210> 37

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)...(32)

<221> CDS

<222> (33)...(740)

<221> 3'UTR

<222> (744)...(970)

<221> sig_peptide

<222> (33)...(92)

<400> 37

gaattcgcag tgccatgaca ccacggggaa cc atg gaa acc cca gcg cag ctt	53
Met Glu Thr Pro Ala Gln Leu	
-20	-15

ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg	101
Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val	
-10	-5
	1

ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc	149
Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala	
5	10
	15

acc ctc tcc tgc agg gcc agt cag agt att agc agc agc tcc tta gcc	197
Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Leu Ala	
20	25
	30
	35

tgg tac cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc ttt ggt	245
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Phe Gly	

40	45	50	
gca tcc agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly 55	60	65	293
tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp 70	75	80	341
ttt gca gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser 85	90	95	389
ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro 100	105	110	437
tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr 120	125	130	485
gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys 135	140	145	533
gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu 150	155	160	581
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser 165	170	175	629
acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala 180	185	190	677
tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe 200	205	210	725
aac agg gga gag tgt tagagggaga agtgccccca cctgctcctc agttccagcc Asn Arg Gly Glu Cys 215			780
tgaccccccctc ccatcctttg gcctctgacc cttttccac aggggaccta cccctattgc ggtcctccag ctcatcttc acctcacccc ctcctcctc cttggctta attatgctaa tgttgagga gaatgaataa ataaagtgaa tctttgcaaa aaaaaaaaaaaa aaaaaaatct ctgcggccgc			840 900 960 970
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 1 5 10 15
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
 Ile Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60
 Pro Gly Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
 100 105 110
 Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
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